

G. DRAPPER

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/399,492A

DATE: 06/08/2000
TIME: 08:10:52

Input Set : A:\903Krev.txt
Output Set: N:\CRF3\06082000\I399492A.raw

#8
JDR

OK
OK

2 <110> APPLICANT: Bazan, J. Fernando
4 <120> TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
6 <130> FILE REFERENCE: DX0903K
8 <140> CURRENT APPLICATION NUMBER: US/09/399,492A
9 <141> CURRENT FILING DATE: 1999-09-20
11 <160> NUMBER OF SEQ ID NOS: 9
13 <170> SOFTWARE: PatentIn Ver. 2.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 468
17 <212> TYPE: DNA
18 <213> ORGANISM: primate
20 <220> FEATURE:
21 <221> NAME/KEY: misc_feature
22 <222> LOCATION: (301)
23 <223> OTHER INFORMATION: nucleotide may be A, C, G, or T
25 <220> FEATURE:
26 <221> NAME/KEY: CDS /
27 <222> LOCATION: (20)..(466)
29 <220> FEATURE:
30 <221> NAME/KEY: mat_peptide
31 <222> LOCATION: (119)..(466)
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34 agtgtgaaac tggggtgga/atg ggg tgt cca cgt atg ttc cct ttt gcc tta 52
35 Met Gly Cys Pro Arg Met Phe Pro Phe Ala Leu
36 -30 -25
38 cta tat gtt ctg tca gtt tct ttc agg aaa atc ttc atc tta caa ctt 100
39 Leu Tyr Val Leu Ser Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu
40 -20 -15 -10
42 gta ggg ctg gtg tta act tac gac ttc act aac tgt gac ttt gag aag 148
43 Val Gly Leu Val Leu Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys
44 -5 -1 1 5 10
46 att aaa gca gcc tat ctc agt act att tct aaa gac ctg att aca tat 196
47 Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr
48 15 20 25
50 atg agt ggg acc aaa agt acc gag ttc aac aac acc gtc tct tgt agc 244
51 Met Ser Gly Thr Lys Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser
52 30 35 40
54 aat cgg cca cat tgc ctt act gaa atc cag agc cta acc ttc aat ccc 292
55 Asn Arg Pro His Cys Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro
56 45 50 55
58 aac cgc cga gtg cgg tgc ctc gcc aaa gaa atg ttc gcc atg aaa act 340
59 Asn Arg Xaa Val Arg Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr
60 60 65 70
62 aag gct gcc tta gct atc tgg tgc cca ggc tat tgc gaa act cag ata 388
63 Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile
64 75 80 85 90
66 aat gct act cag gca atg aag aag agg aga aaa agg aaa gtc aca acc 436

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Input Set : A:\903Krev.txt

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67 Asn Ala Thr Gln Ala Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr
68                               95          100          105
70 aat aaa tgt ctg gaa caa gtg tca caa tta aa                468
71 Asn Lys Cys Leu Gln Val Ser Gln Leu
72                               110          115
75 <210> SEQ ID NO: 2/
76 <211> LENGTH: 149
77 <212> TYPE: PRT
78 <213> ORGANISM: primate
80 <220> FEATURE:
81 <221> NAME/KEY: misc_feature
82 <222> LOCATION: (61)/
83 <223> OTHER INFORMATION: residue will depend on translation of genetic code
85 <400> SEQUENCE: 2
86 Met Gly Cys Pro Arg Met Phe Pro Phe Ala Leu Leu Tyr Val Leu Ser
87                               -30          -25          -20
89 Val Ser Phe Arg Lys Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu
90                               -15          -10          -5
92 Thr Tyr Asp Phe Thr Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr
93  -1  1          5          10          15
95 Leu Ser Thr Ile Ser Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys
96                               20          25          30
98 Ser Thr Glu Phe Asn Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys
99                               35          40          45/
W--> 101 Leu Thr Glu Ile Gln Ser Leu Thr Phe Asn Pro Asn Arg Xaa Val Arg
102                               50          55          60
104 Ser Leu Ala Lys Glu Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala
105                               65          70          75
107 Ile Trp Cys Pro Gly Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala
108  80          85          90          95
109 Met Lys Lys Arg Arg Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu
110                               100          105          110
112 Gln Val Ser Gln Leu
113                               115
115 <210> SEQ ID NO: 3
116 <211> LENGTH: 480
117 <212> TYPE: DNA
118 <213> ORGANISM: primate
120 <220> FEATURE:
121 <221> NAME/KEY: CDS/ /
122 <222> LOCATION: (1)..(477)
124 <220> FEATURE:
125 <221> NAME/KEY: mat_peptide
126 <222> LOCATION: (85)..(477)
128 <400> SEQUENCE: 3
129 atg ttc cct ttt gcc tta cta tat gtt ctg tca gtt tct ttc agg aaa  48
130 Met Phe Pro Phe Ala Leu Leu Tyr Val Leu Ser Val Ser Phe Arg Lys
131                               -25          -20          -15
133 atc ttc atc tta caa ctt gta ggg ctg gtg tta act tac gac ttc act  96

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134 Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu Thr Tyr Asp Phe Thr
135          -10          -5          -1 1
137 aac tgt gac ttt gag aag att aaa gca gcc tat ctc agt act att tct 144
138 Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser
139 5          10          15          20
141 aaa gac ctg att aca tat atg agt ggg acc aaa agt acc gag ttc aac 192
142 Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn
143          25          30          35
145 aac acc gtc tct tgt agc aat cgg cca cat tgc ctt act gaa atc cag 240
146 Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln
147          40          45          50
149 agc cta acc ttc aat ccc acc gcc ggc tgc gcg tcg ctc gcc aaa gaa 288
150 Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu
151          55          60          65
153 atg ttc gcc atg aaa act aag gct gcc tta gct atc tgg tgc cca ggc 336
154 Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly
155          70          75          80
157 tat tcg gaa act cag ata aat gct act cag gca atg aag aag agg aga 384
158 Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met Lys Lys Arg Arg
159 85          90          95          100
161 aaa agg aaa gtc aca acc aat aaa tgt ctg gaa caa gtg tca caa tta 432
162 Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu Gln Val Ser Gln Leu
163          105          110          115
165 caa gga ttg tgg cgt cgc ttc aat cga cct tta ctg aaa caa cag,taa 480
166 Gln Gly Leu Trp Arg Phe Asn Arg Pro Leu Leu Lys Gln Gln
167          120          125          130
168 <210> SEQ ID NO: 4
169 <211> LENGTH: 159
170 <212> TYPE: PRT
171 <213> ORGANISM: primate
173 <400> SEQUENCE: 4
174 Met Phe Pro Phe Ala Leu Leu Tyr Val Leu Ser Val Ser Phe Arg Lys
175          -25          -20          -15
177 Ile Phe Ile Leu Gln Leu Val Gly Leu Val Leu Thr Tyr Asp Phe Thr
178          -10          -5          -1 1
180 Asn Cys Asp Phe Glu Lys Ile Lys Ala Ala Tyr Leu Ser Thr Ile Ser
181 5          10          15          20
183 Lys Asp Leu Ile Thr Tyr Met Ser Gly Thr Lys Ser Thr Glu Phe Asn
184          25          30          35
186 Asn Thr Val Ser Cys Ser Asn Arg Pro His Cys Leu Thr Glu Ile Gln
187          40          45          50
189 Ser Leu Thr Phe Asn Pro Thr Ala Gly Cys Ala Ser Leu Ala Lys Glu
190          55          60          65
192 Met Phe Ala Met Lys Thr Lys Ala Ala Leu Ala Ile Trp Cys Pro Gly
193          70          75          80
195 Tyr Ser Glu Thr Gln Ile Asn Ala Thr Gln Ala Met Lys Lys Arg Arg
196 85          90          95          100
198 Lys Arg Lys Val Thr Thr Asn Lys Cys Leu Glu Gln Val Ser Gln Leu
199          105          110          115

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201 Gln Gly Leu Trp Arg Arg Phe Asn Arg Pro Leu Leu Lys Gln Gln
202      120      125      130
205 <210> SEQ ID NO: 5
206 <211> LENGTH: 176
207 <212> TYPE: PRT
208 <213> ORGANISM: artiodactyla
210 <400> SEQUENCE: 5
211 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
212      1      5      10      15
214 Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Phe Ser Gly Lys
215      20      25      30
217 Asp Gly Gly Ala Tyr Gln Asn Val Leu Met Val Ser Ile Asp Asp Leu
218      35      40      45
220 Asp Asn Met Ile Asn Phe Asp Ser Asn Cys Leu Asn Asn Glu Pro Asn
221      50      55      60
223 Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
224      65      70      75      80
226 Asn Arg Ala Ala Arg Lys Leu Lys Gln Phe Leu Lys Met Asn Ile Ser
227      85      90      95
229 Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
230      100     105     110
232 Leu Leu Asn Cys Thr Ser Lys Gly Lys Gly Arg Lys Pro Pro Ser Leu
233      115     120     125
235 Gly Glu Ala Gln Pro Thr Lys Asn Leu Glu Glu Asn Lys Ser Leu Lys
236      130     135     140
238 Glu Gln Arg Lys Gln Asn Asp Leu Cys Phe Leu Lys Ile Leu Leu Gln
239      145     150     155     160
241 Lys Ile Lys Thr Cys Trp Asn Lys Ile Leu Arg Gly Ile Thr Glu His
242      165     170     175
248 <210> SEQ ID NO: 6
249 <211> LENGTH: 176
250 <212> TYPE: PRT
251 <213> ORGANISM: artiodactyla
253 <400> SEQUENCE: 6
254 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
255      1      5      10      15
257 Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Ser Gly Lys
258      20      25      30
260 Asp Gly Gly Ala Tyr Gln Asn Val Leu Met Val Asn Ile Asp Asp Leu
261      35      40      45
263 Asp Asn Met Ile Asn Phe Asp Ser Asn Cys Leu Asn Asn Glu Pro Asn
264      50      55      60
266 Phe Phe Lys Lys His Ser Cys Asp Asp Asn Lys Glu Ala Ser Phe Leu
267      65      70      75      80
269 Asn Arg Ala Ser Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ile Ser
270      85      90      95
272 Asp Asp Phe Lys Leu His Leu Ser Thr Val Ser Gln Gly Thr Leu Thr
273      100     105     110
275 Leu Leu Asn Cys Thr Ser Lys Gly Lys Gly Arg Lys Pro Pro Ser Leu

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276          115          120          125
278 Ser Glu Ala Gln Pro Thr Lys Asn Leu Glu Glu Asn Lys Ser Ser Lys
279          130          135          140
281 Glu Gln Lys Lys Gln Asn Asp Leu Cys Phe Leu Lys Ile Leu Leu Gln
282 145          150          155          160
284 Lys Ile Lys Thr Cys Trp Asn Lys Ile Leu Arg Gly Ile Lys Glu His
285          165          170          175
289 <210> SEQ ID NO: 7
290 <211> LENGTH: 177
291 <212> TYPE: PRT
292 <213> ORGANISM: primate
294 <400> SEQUENCE: 7
295 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Leu Pro Pro Leu Ile
296   1          5          10          15
298 Leu Val Leu Leu Pro Val Ala Ser Ser Asp Cys Asp Ile Glu Gly Lys
299          20          25          30
301 Asp Gly Lys Gln Tyr Glu Ser Val Leu Met Val Ser Ile Asp Gln Leu
302          35          40          45
304 Leu Asp Ser Met Lys Glu Ile Gly Ser Asn Cys Leu Asn Asn Glu Phe
305          50          55          60
307 Asn Phe Phe Lys Arg His Ile Cys Asp Ala Asn Lys Glu Gly Met Phe
308          65          70          75          80
310 Leu Phe Arg Ala Ala Arg Lys Leu Arg Gln Phe Leu Lys Met Asn Ser
311          85          90          95
313 Thr Gly Asp Phe Asp Leu His Leu Leu Lys Val Ser Glu Gly Thr Thr
314          100          105          110
316 Ile Leu Leu Asn Cys Thr Gly Gln Val Lys Gly Arg Lys Pro Ala Ala
317          115          120          125
319 Leu Gly Glu Ala Gln Pro Thr Lys Ser Leu Glu Glu Asn Lys Ser Leu
320          130          135          140
322 Lys Glu Gln Lys Lys Leu Asn Asp Leu Cys Phe Leu Lys Arg Leu Leu
323 145          150          155          160
325 Gln Glu Ile Lys Thr Cys Trp Asn Lys Ile Leu Met Gly Thr Lys Glu
326          165          170          175
328 His
332 <210> SEQ ID NO: 8
333 <211> LENGTH: 154
334 <212> TYPE: PRT
335 <213> ORGANISM: rodent
337 <400> SEQUENCE: 8
338 Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
339   1          5          10          15
341 Leu Val Leu Leu Pro Val Thr Ser Ser Glu Cys His Ile Lys Asp Lys
342          20          25          30
344 Glu Gly Lys Ala Tyr Glu Ser Val Leu Met Ile Ser Ile Asp Glu Leu
345          35          40          45
347 Asp Lys Met Thr Gly Thr Asp Ser Asn Cys Pro Asn Asn Glu Pro Asn
348          50          55          60
350 Phe Phe Arg Lys His Val Cys Asp Asp Thr Lys Glu Ala Ala Phe Leu

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VERIFICATION SUMMARY DATE: 06/08/2000
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Input Set : A:\903Krev.txt
 Output Set: N:\CRF3\06082000\I399492A.raw

OK
 L:8 M:270 C: Current Application Number differs, Replaced Application Number
 L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
 L:102 M:283 W: Missing Blank Line separator, <210> field identifier